

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,583C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH104.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
US-08-335-583C-47

Query Match 100.0%; Score 111; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLAIS 20
Db 57 INPETYKPCCAPTQNLAIS 76

RESULT 3
US-08-288-508C-18
Sequence 18, Application US/08288508C
Patent No. 5994094
GENERAL INFORMATION:
APPLICANT: H. Iken, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
TITLE OF INVENTION: THE TGF- FAMILY
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,508C
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 26 829.3
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 18 222.8
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 20 157.5
FILING DATE: 09-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: JAHNS, Kristina M.
REGISTRATION NUMBER: P-41,092
REFERENCE/DOCKET NUMBER: P564-4019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-288-508C-18

Query Match 100.0%; Score 111; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLAIS 20
Db 57 INPETYKPCCAPTQNLAIS 76

RESULT 4
US-08-478-097A-16
Sequence 16, Application US/08478097A
Patent No. 6040431
GENERAL INFORMATION:
APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBAUT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,097A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDWARD R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..102

OTHER INFORMATION: /note= "OP-1 SEQUENCE"
US-08-478-097A-16

Query Match 100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETHKPCCAPTOLNAIS 20
Db 57 INPETHKPCCAPTOLNAIS 76

RESULT 5
US-08-289-222E-27
Sequence 27, Application US/08289222E
Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-222E-27
Query Match 100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETHKPCCAPTOLNAIS 20
Db 57 INPETHKPCCAPTOLNAIS 76

RESULT 6
US-09-054-526B-27
Sequence 27, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H TTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-526B-27
Query Match 100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETHKPCCAPTOLNAIS 20
Db 57 INPETHKPCCAPTOLNAIS 76

RESULT 7
US-08-931-858E-161
Sequence 161, Application US/08931858E

Patent No. 6222022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-931-858B-161

Query Match 100.0%; Score 111; DB 3; Length 102;
Best local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPEYVKPCCAPTOINAI 20
DB 57 INPEYVKPCCAPTOINAI 76

RESULT 8
US-08-981-739-161
Sequence 161, Application US/08981739
Patent No. 6232449
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/03461
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 161:
US-08-981-739-161

Query Match 100.0%; Score 111; DB 3; Length 102;
Best local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPEYVKPCCAPTOINAI 20
DB 57 INPEYVKPCCAPTOINAI 76

RESULT 9
US-08-786-284A-1
Sequence 1, Application US/08786284A
Patent No. 6273598
GENERAL INFORMATION:
APPLICANT: KECK, PETER
APPLICANT: GRIFFITH, DIANA L
APPLICANT: CARLSON, WILLIAM D
APPLICANT: RUGGER, DAVID C
APPLICANT: SAMPATH, KUBER T
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
ADDRESS: INC
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,284A
FILING DATE:
CLASSIFICATION: 364
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDWARD R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-0992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..102
OTHER INFORMATION: /product= "NOP-1"
US-08-786-284A-1

Query Match 100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLNALS 20
DB 57 INPETYKPCCAPTQNLNALS 76

RESULT 10
US-09-128-026-161
Sequence 161, Application US/09128026
Patent No. 6403335
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,026
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-128-026-161

Query Match 100.0%; Score 111; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLNALS 20
DB 57 INPETYKPCCAPTQNLNALS 76

RESULT 11

US-09-496-398-16
Sequence 16, Application US/09496398
Patent No. 6479643
GENERAL INFORMATION:
APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HIRWITZ &
ADDRESSEE: THIBEAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/496,398
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,097
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-059CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..102
OTHER INFORMATION: /note= "OP-1 SEQUENCE"
US-09-496-398-16

Query Match 100.0%; Score 111; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLNALS 20
DB 57 INPETYKPCCAPTQNLNALS 76

RESULT 12
US-09-220-616-161
Sequence 161, Application US/09220616
Patent No. 6645937
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400

CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
APPLICATION NUMBER: PCT/US97/03461
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-220-616-161

Query Match 100.0%; Score 111; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLAI 20
DB 57 INPETYKPCCAPTQNLAI 76

RESULT 13
US-09-374-958C-55
Sequence 55, Application US/09374958C
Patent No. 6677432
GENERAL INFORMATION:
APPLICANT: Striker Corporation
TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
FILE REFERENCE: STX-076
CURRENT APPLICATION NUMBER: US/09/374,958C
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 2.0
SEQ ID NO 55
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: OP-1
US-09-374-958C-55

Query Match 100.0%; Score 111; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLAI 20
DB 57 INPETYKPCCAPTQNLAI 76

RESULT 14
US-07-764-731B-8
Sequence 8, Application US/0764731B
Patent No. 536875
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Wang, Elizabeth A.
APPLICANT: Mooney, John M.
TITLE OF INVENTION: Methods for Producing BMP-7 Proteins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/764,731B
FILING DATE: 19910924
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: G15159B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-764-731B-8

Query Match 100.0%; Score 111; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLAI 20
DB 59 INPETYKPCCAPTQNLAI 78

RESULT 15
US-09-374-958C-69
Sequence 69, Application US/09374958C
Patent No. 6677432
GENERAL INFORMATION:
APPLICANT: Striker Corporation
TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
FILE REFERENCE: STX-076
CURRENT APPLICATION NUMBER: US/09/374,958C
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 2.0
SEQ ID NO 69
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Trypsin truncated H2223 mutant
US-09-374-958C-69

Query Match 100.0%; Score 111; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;

Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	INPETYKPKCAPTQLNIAIS	20						
Db	72	INPETYKPKCAPTQLNIAIS	91						

Search completed: October 12, 2004, 09:38:46
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: October 12, 2004, 09:37:49 ; Search time 96 Seconds
(without alignments)
67.041 Million cell updates/sec

Title: US-10-619-910-11

Perfect score: 111

Sequence: 1 INPETHKPCCAPTQNAIS 20

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_Aa.*

1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpa/PCCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/1/pubpa/PCCT_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpa/US09C_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	100.0	20	12	US-10-619-910-11
2	111	100.0	97	11	US-09-754-831A-39
3	111	100.0	102	9	US-09-791-946-1
4	111	100.0	102	14	US-10-187-394-16
5	111	100.0	102	14	US-10-164-279-4
6	111	100.0	107	11	US-09-754-831A-9
7	111	100.0	112	9	US-09-813-398-30
8	111	100.0	118	13	US-10-115-406-10
9	111	100.0	118	14	US-10-154-333-12
10	111	100.0	118	16	US-10-704-223-10
11	111	100.0	119	9	US-09-813-453-13
12	111	100.0	119	9	US-09-859-211-40
13	111	100.0	119	9	US-09-880-708-18
14	111	100.0	119	10	US-09-872-856-40
15	111	100.0	119	12	US-10-463-973-40

16	111	100.0	119	12	US-10-693-536-12	Sequence 12, Appl
17	111	100.0	119	14	US-10-333-493-22	Sequence 22, Appl
18	111	100.0	119	16	US-10-758-210-12	Sequence 12, Appl
19	111	100.0	139	8	US-08-260-675-5	Sequence 5, Appl
20	111	100.0	139	9	US-09-882-875A-1	Sequence 1, Appl
21	111	100.0	139	12	US-09-952-318A-5	Sequence 5, Appl
22	111	100.0	139	12	US-10-366-345-63	Sequence 63, Appl
23	111	100.0	139	14	US-10-050-050-5	Sequence 5, Appl
24	111	100.0	139	15	US-10-108-260A-2783	Sequence 2783, Ap
25	111	100.0	139	16	US-10-385-064-5	Sequence 5, Appl
26	111	100.0	161	9	US-09-765-527-249	Sequence 249, App
27	111	100.0	161	9	US-09-760-397-2	Sequence 2, Appl
28	111	100.0	161	14	US-10-324-182-2	Sequence 2, Appl
29	111	100.0	169	8	US-08-957-425-9	Sequence 9, Appl
30	111	100.0	169	12	US-10-321-799-9	Sequence 9, Appl
31	111	100.0	169	16	US-10-428-997A-9	Sequence 9, Appl
32	111	100.0	178	9	US-09-760-397-8	Sequence 8, Appl
33	111	100.0	178	14	US-10-324-182-8	Sequence 8, Appl
34	111	100.0	179	9	US-09-765-527-257	Sequence 257, App
35	111	100.0	179	9	US-09-765-527-261	Sequence 261, App
36	111	100.0	190	9	US-09-760-397-14	Sequence 14, Appl
37	111	100.0	190	14	US-10-324-182-14	Sequence 14, Appl
38	111	100.0	194	9	US-09-765-527-235	Sequence 235, App
39	111	100.0	195	9	US-09-765-527-263	Sequence 263, App
40	111	100.0	317	8	US-08-957-425-11	Sequence 11, Appl
41	111	100.0	317	12	US-10-321-799-11	Sequence 11, Appl
42	111	100.0	317	16	US-10-428-997A-11	Sequence 15, Appl
43	111	100.0	408	8	US-08-957-425-15	Sequence 15, Appl
44	111	100.0	408	12	US-10-321-799-15	Sequence 15, Appl
45	111	100.0	408	16	US-10-428-997A-15	Sequence 15, Appl

ALIGNMENTS

```

RESULT 1
US-10-619-910-11
; Sequence 11, Application US/10619910
; Publication No. US20040053844A1
; GENERAL INFORMATION:
; APPLICANT: Kyocera Corporation
; APPLICANT: Nishimura, Yoshihiko
; APPLICANT: Suzuki, Yoshihisa
; APPLICANT: Tanihara, Masao
; TITLE OF INVENTION: A peptide and Osteogenic Accelerator
; FILE REFERENCE: 81918-0001
; CURRENT APPLICATION NUMBER: US/10/619,910
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/439,779B
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
; US-10-619-910-11

Query Match      100.0%; Score 111; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox      1 INPETHKPCCAPTQNAIS 20
Db      1 INPETHKPCCAPTQNAIS 20

RESULT 2
US-09-754-831A-39
; Sequence 39, Application US/09754831A
; Publication No. US20030228345A1

```

GENERAL INFORMATION:
APPLICANT: Oppermann, Herman
APPLICANT: Kuberampath, Thangavel
APPLICANT: Rueger, David
APPLICANT: Ozkaynak, Engin
TITLE OF INVENTION: Osteogenic Devices
FILE REFERENCE: STK-008CN
CURRENT APPLICATION NUMBER: US/09/754,831A
CURRENT FILING DATE: 2001-01-03
PRIORITY APPLICATION NUMBER: US 08/375,901
PRIORITY FILING DATE: 1995-01-20
PRIORITY APPLICATION NUMBER: US 08/145,812
PRIORITY FILING DATE: 1993-11-01
PRIORITY APPLICATION NUMBER: US 07/995,345
PRIORITY FILING DATE: 1993-12-22
PRIORITY APPLICATION NUMBER: US 07/315,342
PRIORITY FILING DATE: 1988-02-23
PRIORITY APPLICATION NUMBER: US 07/232,630
PRIORITY FILING DATE: 1988-08-15
PRIORITY APPLICATION NUMBER: US 07/179,406
PRIORITY FILING DATE: 1988-04-08
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 39
LENGTH: 97
TYPE: PRT
ORGANISM: mammalian
FEATURE:
OTHER INFORMATION: OPI shorter sequence capable of inducing endochondral bone format
US-09-754-831A-39

Query Match 100.0%; Score 111; DB 11; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLALS 20
DB 52 INPETYKPCCAPTQNLALS 71

RESULT 3
US-09-791-946-1
Sequence 1, Application US/09791946
Patent No. US20020028453A1
GENERAL INFORMATION:
APPLICANT: KECK, PETER
GRIFFITH, DIANA L
CARLSON, WILLIAM D
RUEGER, DAVID C
SAMPATH, KUBER T
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
MORPHOGEN ANALOGS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/791,946
FILING DATE: 22-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/766,284
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-0992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..102
OTHER INFORMATION: /product= "hGF-1"
US-09-791-946-1

Query Match 100.0%; Score 111; DB 9; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNLALS 20
DB 57 INPETYKPCCAPTQNLALS 76

RESULT 4
US-10-187-394-16
Sequence 16, Application US/10187394
Publication No. US20030176667A1
GENERAL INFORMATION:
APPLICANT: KECK, PETER
SMART, JOHN
TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHOGENS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESS: THIBAUDT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/187,394
FILING DATE: 28-JUNE-2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/496,398
FILING DATE: 02-FEB-2000
CLASSIFICATION:
APPLICATION NUMBER: US 08/478,097
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-059CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7100
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..102
OTHER INFORMATION: /note= "CP-1 SEQUENCE"
US-10-187-394-16

Query Match 100.0%; Score 111; DB 14; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPTQLNALS 20
DB 57 INPETHKPCCAPTQLNALS 76

RESULT 5
US-10-164-279-4
Sequence 4, Application US/10164279
Publication No. US20030185792A1
GENERAL INFORMATION:
APPLICANT: Keck, P.
TITLE OF INVENTION: MORPHOGEN ANALOGS OF BOND MORPHOGENIC PROTEINS
FILE REFERENCE: CIBT-P04-566
CURRENT APPLICATION NUMBER: US/10/164,279
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 09/791946
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
US-10-164-279-4

Query Match 100.0%; Score 111; DB 14; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPTQLNALS 20
DB 57 INPETHKPCCAPTQLNALS 76

RESULT 6
US-09-754-831A-9
Sequence 9, Application US/09754831A
Publication No. US20030228345A1
GENERAL INFORMATION:
APPLICANT: Oppermann, Herman
APPLICANT: Kuberassampath, Thangavel
APPLICANT: Rueger, David
APPLICANT: Ozkaynak, Engin
TITLE OF INVENTION: Osteogenic Devices
FILE REFERENCE: STK-0086N
CURRENT APPLICATION NUMBER: US/09/754,831A
CURRENT FILING DATE: 2001-01-03
PRIOR APPLICATION NUMBER: US 08/375,901
PRIOR FILING DATE: 1995-01-20
PRIOR APPLICATION NUMBER: US 08/145,812
PRIOR FILING DATE: 1993-11-01
PRIOR APPLICATION NUMBER: US 07/995,345
PRIOR FILING DATE: 1992-12-22
PRIOR APPLICATION NUMBER: US 07/315,342
PRIOR FILING DATE: 1989-02-23
PRIOR APPLICATION NUMBER: US 07/232,630
PRIOR FILING DATE: 1988-08-15
PRIOR APPLICATION NUMBER: US 07/179,406

PRIOR FILING DATE: 1988-04-08
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 107
TYPE: PRT
ORGANISM: mammalian
FEATURE:
OTHER INFORMATION: OPI protein sequence with osteogenic activity
US-09-754-831A-9

Query Match 100.0%; Score 111; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPTQLNALS 20
DB 62 INPETHKPCCAPTQLNALS 81

RESULT 7
US-09-813-398-30
Sequence 30, Application US/09813398
Patent No. US20030169292A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Skudlinski
APPLICANT: University of Maryland
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REFERENCE: USFMD-003C1
CURRENT APPLICATION NUMBER: US/09/813,398
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/US98/19772
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 112
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-813-398-30

Query Match 100.0%; Score 111; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPTQLNALS 20
DB 68 INPETHKPCCAPTQLNALS 87

RESULT 8
US-10-115-406-10
Sequence 10, Application US/10115406
Publication No. US20020127612A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: Lee, Se-uh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
FILE REFERENCE: JHU1190-3
CURRENT APPLICATION NUMBER: US/10/115,406
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/301,520
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: US 09/172,062
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/491,835
PRIOR FILING DATE: 1995-10-23
PRIOR APPLICATION NUMBER: PCT/US94/00685
PRIOR FILING DATE: 1994-01-12
PRIOR APPLICATION NUMBER: US 08/003,303

PRIOR FILING DATE: 1993-01-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO: 10
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-406-10

Query Match 100.0%; Score 111; DB 13; Length 118;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 INPETYKPCCAPTOLNAIS 20
DB 73 INPETYKPCCAPTOLNAIS 92

RESULT 9
US-10-154-333-12

Sequence 12, Application US/10154333
Publication No. US20030109684A1

GENERAL INFORMATION:

APPLICANT: JOHNS HOPKINS UNIVERSITY

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ

STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR

CITY: LOS ANGELES

STATE: CALIFORNIA

COUNTRY: US

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/154,333

FILING DATE: 21-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/389,705

FILING DATE: 03-Sep-1999

APPLICATION NUMBER: 09/153,733

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WETHERELL, JR. Ph.D., JOHN R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: PD2279 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

IMMEDIATE SOURCE:

CLONE: OP-1

FEATURE:

NAME/KEY: Protein

LOCATION: 1..118

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-154-333-12

Query Match 100.0%; Score 111; DB 14; Length 118;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 INPETYKPCCAPTOLNAIS 20
DB 73 INPETYKPCCAPTOLNAIS 92

RESULT 10
US-10-704-223-10

Sequence 10, Application US/10704223
Publication No. US20040152143A1

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY

APPLICANT: LEE, Se-Jin

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9

FILE REFERENCE: JHU1190-7

CURRENT APPLICATION NUMBER: US/10/704,223

CURRENT FILING DATE: 2003-11-07

PRIOR APPLICATION NUMBER: US 10/115,406

PRIOR FILING DATE: 2002-04-02

PRIOR APPLICATION NUMBER: US 09/301,520

PRIOR FILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: US 09/172,062

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: US 08/491,835

PRIOR FILING DATE: 1995-10-23

PRIOR APPLICATION NUMBER: PCT/US94/00685

PRIOR FILING DATE: 1994-01-12

PRIOR APPLICATION NUMBER: US 08/003,303

PRIOR FILING DATE: 1993-01-12

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1

SEQ ID NO: 10

LENGTH: 118

TYPE: PRT

ORGANISM: Homo sapiens

US-10-704-223-10

Query Match 100.0%; Score 111; DB 16; Length 118;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 INPETYKPCCAPTOLNAIS 20
DB 73 INPETYKPCCAPTOLNAIS 92

RESULT 11

US-09-813-459-13

Sequence 13, Application US/09813459

Patent No. US20020107369A1

GENERAL INFORMATION:

APPLICANT: Lee, Se-Jin

Cummingham, NC, US20020107369A1

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Spensley Horn Jubas & Lubitz

STREET: 1880 Century Park East, Suite 500

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/813,459

FILING DATE: 20-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/624,635

FILING DATE: <Unknown>

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ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: OP-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-813-459-13

Query Match      100.0%; Score 111; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNAIS 20
DB 74 INPETYKPCCAPTQNAIS 93

RESULT 12
US-09-859-211-40
Sequence 40, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-211-40

Query Match      100.0%; Score 111; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 13
US-09-880-708-18
Sequence 18, Application US/09880708
Patent No. US20020165361A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/145,060
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Halle, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 619/677-1465
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: OP-1
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-880-708-18

Query Match      100.0%; Score 111; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETYKPCCAPTQNAIS 20
DB 74 INPETYKPCCAPTQNAIS 93

RESULT 14
US-09-872-856-40
Sequence 40, Application US/09872856
Patent No. US20030074680A1
GENERAL INFORMATION:
APPLICANT: Johns Hopkins University School of Medicine
APPLICANT: Lee, Se-jin
APPLICANT: McPherron, Alexandra
TITLE OF INVENTION: Growth Differentiation Factor-8
FILE REFERENCE: JHU1120-17
CURRENT APPLICATION NUMBER: US/09/872,856
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 09/124,180
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: US 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: US 08/862,445
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Search completed: October 12, 2004, 09:45:49
Job time : 97 secs

PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: US 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 08/525,596
PRIOR FILING DATE: 1995-10-25
PRIOR APPLICATION NUMBER: PCT/US 94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: US 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 40
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-09-872-856-40

Query Match 100.0%; Score 111; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 INPETHKPCCAPTOLNAIS 20
Db 74 INPETHKPCCAPTOLNAIS 93

RESULT 15
US-10-463-973-40
Sequence 40, Application US/10463973
Publication No. US20040055027A1
GENERAL INFORMATION:
APPLICANT: Johns Hopkins University School of Medicine
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra
TITLE OF INVENTION: Growth Differentiation Factor-8
FILE REFERENCE: JH01120-17
CURRENT APPLICATION NUMBER: US/10/463,973
CURRENT FILING DATE: 2003-06-17
PRIOR APPLICATION NUMBER: US/09/872,856
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 09/124,180
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: US 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: US 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: US 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 08/525,596
PRIOR FILING DATE: 1995-10-25
PRIOR APPLICATION NUMBER: PCT/US 94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: US 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 40
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-10-463-973-40

Query Match 100.0%; Score 111; DB 12; Length 119;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 INPETHKPCCAPTOLNAIS 20
Db 74 INPETHKPCCAPTOLNAIS 93

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 12, 2004, 09:10:03 / Search time 30 Seconds
(without alignments)
64.128 Million cell updates/sec

Title: US-10-619-910-11
Perfect score: 111
Sequence: 1 INPETHPKPCAPQLNLAIS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	100.0	313	2	151284
2	111	100.0	431	1	BMH07
3	108	97.3	430	2	JQ1184
4	107	96.4	426	2	JH0690
5	97	87.4	207	2	S37618
6	97	87.4	510	2	AS4798
7	97	87.4	513	1	BMH05
8	87	78.4	452	2	149542
9	87	78.4	454	1	BMH05
10	84	75.7	34	2	A36626
11	77	69.4	455	2	A43918
12	71	64.0	360	2	A29619
13	71	64.0	588	2	A26158
14	70	63.1	402	2	A45056
15	70	63.1	461	2	S52408
16	64	57.7	365	2	T43286
17	64	57.7	400	2	A49147
18	64	57.7	401	2	JH0689
19	64	57.7	405	2	I50608
20	64	57.7	408	1	BMH04
21	64	57.7	408	2	JH0801
22	64	57.7	408	2	S38343
23	64	57.7	408	2	S58791
24	64	57.7	420	2	149541
25	64	57.7	427	2	A40735
26	63	56.8	309	2	JC5697
27	63	56.8	353	2	I50607
28	63	56.8	393	2	S37073
29	63	56.8	394	2	S45355

30	63	56.8	396	1	BMH02	bone morphogenetic
31	63	56.8	398	2	JH0688	bone morphogenetic
32	63	56.8	398	2	JH0687	bone morphogenetic
33	63	56.8	495	2	S43294	bone morphogenetic
34	63	56.8	501	2	AS5452	cartilage-derived
35	63	56.8	501	2	JC2347	growth/differentia
36	55	49.5	125	2	S43295	bone morphogenetic
37	55	49.5	436	2	B55452	bone morphogenetic
38	54	48.6	409	2	S01825	cartilage-derived
39	54	48.6	410	2	A41397	transforming growth
40	54	48.6	410	2	AS5706	transforming growth
41	54	48.6	412	2	A36165	transforming growth
42	54	48.6	412	2	A34939	transforming growth
43	54	48.6	413	2	JC4862	activin beta-A cha
44	54	48.6	476	2	JC4646	bone morphogenetic
45	54	48.6	478	2	JC4838	bone morphogenetic

ALIGNMENTS

RESULT 1
151284
bone morphogenetic protein-7 - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C/Accession: 151284
R/Houston, B.; Thorp, B.H.; Burt, D.W.
J. Mol. Endocrinol. 13, 289-301, 1994
A/Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick e
A/Reference number: 151284, MUID:55200473, PMID:7893347
A/Accession: 151284
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-313 <HOU>
A/Cross-references: GB:S77477; NID:9357233; PIDN:AA83846.1; PID:9357234
C/Superfamily: inhibin

Query Match 100.0%; Score 111; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 INPETHPKPCAPQLNLAIS 20
Db 268 INPETHPKPCAPQLNLAIS 267

RESULT 2
BMH07
bone morphogenetic protein 7 precursor - human
C/Alternate names: osteogenic protein 1
C/Species: Homo sapiens (man)
C/Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C/Accession: C39263; S10529
R/Celesia, A.U.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozn
Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A/Title: Identification of a transforming growth factor beta family members present in bon
A/Reference number: A39263; MUID:91088608; PMID:22833636
A/Accession: C39263
A/Molecule type: mRNA
A/Residues: 1-431 <CEL>
A/Cross-references: GB:M60316; GB:M38695; NID:9339563; PIDN:AAA6738.1; PID:9339564
R/Oezkaynak, E.; Rueger, D.C.; Drier, E.A.; Corbett, C.; Ridge, R.J.; Sampath, T.K.; Opp
EMBO J. 9, 2085-2093, 1990
A/Title: OP-1 cDNA encodes an osteogenic protein in the TGF-beta family.
A/Reference number: S10529; MUID:90291971; PMID:2357959
A/Accession: S10529
A/Molecule type: mRNA
A/Residues: 1-431 <OEZ>
A/Cross-references: EMBL:X51801; NID:935151; PIDN:CAA36100.1; PID:935152
C/Genetics:
A/Gene: GDB:BMP7
A/Cross-references: GDB:127597; OMIM:112267

A:Map position: 20pter-20qter
C:Superfamily: Inhibin
C:Keywords: bone; dimer; glycoprotein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-299/Domain: propeptide #status predicted <PRO>
F:300-431/Product: bone morphogenetic protein 7 #status predicted <MAT>
F:187,302,372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 111; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1,3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPEYVPRKPCAPTOINAI 20
DB 386 INPEYVPRKPCAPTOINAI 405

RESULT 3

QJ1184
osteogenic protein 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
C/Accession: QJ1184; P00224
R:Oezkaynak, E.; Schneegelsberg, P.N.J.; Oppermann, H.
Biochem. Biophys. Res. Commun. 179, 116-123, 1991
A>Title: Murine osteogenic protein (OP-1): high levels of mRNA in kidney.
A:Reference number: QJ1184; PMID:91354237; PMID:1715687
A:Accession: J01184
A:Molecule type: DNA
A:Residues: 1-120 <OEZ>
A:Cross-references: EMBL:X56906
A:Accession: P00224
A:Molecule type: mRNA
A:Residues: 54-430 <OEZ>
C:Comment: This protein induces bone formation.
C:Superfamily: Inhibin
C:Keywords: glycoprotein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-290/Domain: propeptide #status predicted <PRO>
F:291-430/Product: osteogenic protein-1 #status predicted <MAT>
F:186,301,320,371/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.3%; Score 108; DB 2; Length 430;
Best Local Similarity 95.0%; Pred. No. 3.6e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPEYVPRKPCAPTOINAI 20
DB 385 INPEYVPRKPCAPTOINAI 404

RESULT 4
JH0690
bone morphogenetic protein 7 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C/Accession: JH0690
R:Yoshimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A>Title: Genes for bone morphogenetic proteins are differentially transcribed in early
A:Reference number: JH0687; PMID:92378616; PMID:1510675
A:Accession: JH0690
A:Molecule type: mRNA
A:Residues: 1-426 <NIS>
A:Cross-references: GB:X63427; NID:964591; PIDN:CAA5021.1; PID:964592
A:Experimental source: oocyte
C:Superfamily: Inhibin
C:Keywords: glycoprotein
F:283-426/Product: bone morphogenetic protein 7 #status predicted <MAT>
F:177,307,367/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.4%; Score 107; DB 2; Length 426;
Best Local Similarity 95.0%; Pred. No. 4.9e-08;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPEYVPRKPCAPTOINAI 20
DB 381 INPEYVPRKPCAPTOINAI 400

RESULT 5
S37618
vgr protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
C/Accession: S37618
R:Saetermann, U.; Meyerann, R.; Schluessener, H.J.
J. Neurosci. Res. 33, 142-147, 1992
A>Title: Cloning of a novel tgf-beta related cytokine, the vgr, from rat brain: cloning
A:Reference number: S37618; PMID:93085758; PMID:1453478
A:Accession: S37618
A:Molecule type: mRNA
A:Residues: 1-207 <SAU>
A:Cross-references: EMBL:X58830; NID:957475; PIDN:CAA41634.1; PID:957476
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser
C:Superfamily: Inhibin

Query Match 87.4%; Score 97; DB 2; Length 207;
Best Local Similarity 85.0%; Pred. No. 7.3e-07;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPEYVPRKPCAPTOINAI 20
DB 162 INPEYVPRKPCAPTOINAI 181

RESULT 6
A54798
Vg-1-related protein precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C/Accession: A54798; A33925; S47442
R:Glitsman, S.E.; Koblin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.
J. Cell Biol. 126, 1595-1609, 1994
A>Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral bone
A:Reference number: A54798; PMID:94375533; PMID:8089189
A:Accession: A54798
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-510 <GIT>
A:Cross-references: EMBL:X80992; NID:9530729; PIDN:CAA56917.1; PID:9530730
R:Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, B.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
A>Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the transforming
A:Reference number: A33925; PMID:89282810; PMID:2734307
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 'M', 74, 'K', 76-85, 'P', 87-510 <LYO>
A:Cross-references: GB:J04566; NID:9202352; PIDN:AAA40548.1; PID:9202353
C:Superfamily: Inhibin

Query Match 87.4%; Score 97; DB 2; Length 510;
Best Local Similarity 85.0%; Pred. No. 1.7e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPEYVPRKPCAPTOINAI 20
DB 465 INPEYVPRKPCAPTOINAI 484

RESULT 7
BMH16
bone morphogenetic protein 6 precursor - human
C:Species: Homo sapiens (man)

C>Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C/Accession: B39263
 R/Celeste: A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozni
 Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
 A>Title: Identification of transforming factor beta family members present in bot
 A/Reference number: A39263; MUID:91088608; PMID:2263636
 A/Accession: B39263
 A/Molecule type: mRNA
 A/Residues: 1-513 <CEL>
 A/Cross-references: GB:M60315; GB:M38694; NID:g339556; PIDN:AAA36737.1; PID:g339562
 C/Genetics:
 A/Gene: GDB:BMP6
 A/Cross-references: GDB:127596; OMIM:112266
 A/Map position: 6pter-6qter
 C/Superfamily: inhibin
 C/Keywords: bone; glycoprotein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-374/Domain: propeptide #status predicted <PRO>
 F:375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
 F:241,269,386,404,454/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 97; DB 1; Length 513;
 Best Local Similarity 85.0%; Pred. No. 1.7e-06;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 INPETHKPCCAPTQNLMAIS 20
 :|||||
 Db 468 NMDEVKPCCAPTKLMAIS 487

RESULT 8
 149542
 bone morphogenetic protein 5 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 C/Accession: 149542
 R/King, J.A.; Marker, P.C.; Seung, K.U.; Kingsley, D.M.
 Dev. Biol. 166, 112-122, 1994
 A>Title: BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice
 A/Reference number: 149542; MUID:95046894; PMID:7958439
 A/Accession: 149542
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-452 <RES>
 A/Cross-references: GB:I41145; NID:g755033; PIDN:AAA64612.1; PID:g755034
 C/Genetics:
 A/Gene: BMP5
 C/Superfamily: inhibin

Query Match 78.4%; Score 87; DB 2; Length 452;
 Best Local Similarity 83.3%; Pred. No. 4.2e-05;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PETVXPCCAPTLQNLMAIS 20
 :|||||
 Db 409 PDHVPKPCCAPTKLMAIS 426

RESULT 9
 BMH05
 bone morphogenetic protein 5 precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C/Accession: A39263
 R/Celeste, A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozni
 Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
 A>Title: Identification of transforming factor beta family members present in bot
 A/Reference number: A39263; MUID:91088608; PMID:2263636
 A/Accession: A39263
 A/Molecule type: mRNA
 A/Residues: 1-454 <CEL>
 A/Cross-references: GB:M60314; GB:M38693; NID:g339559; PIDN:AAA36736.1; PID:g339560
 C/Genetics:

A/Gene: GDB:BMP5
 A/Cross-references: GDB:127595; OMIM:112265
 A/Map position: 6pter-6qter
 C/Superfamily: inhibin
 C/Keywords: bone; glycoprotein
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-316/Domain: propeptide #status predicted <PRO>
 F:317-454/Product: bone morphogenetic protein 5 #status predicted <MAT>
 F:211,327,345,395/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 78.4%; Score 87; DB 1; Length 454;
 Best Local Similarity 83.3%; Pred. No. 4.3e-05;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 PETVXPCCAPTLQNLMAIS 20
 :|||||
 Db 411 PDHVPKPCCAPTKLMAIS 428

RESULT 10
 A36626
 osteogenic protein 18K chain - bovine (fragments)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 03-May-1996
 C/Accession: A36626
 R/Sampath, T.K.; Coughlin, J.E.; Whetstone, R.M.; Banach, D.; Corbett, C.; Ridge, R.J.;
 J. Biol. Chem. 265, 13198-13205, 1990
 A>Title: Bovine osteogenic protein is composed of dimers of OP-1 and BMP-2A, two members
 A/Reference number: A36626; MUID:90330665; PMID:2376552
 A/Accession: A36626
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-34 <SAM>
 C/Superfamily: inhibin

Query Match 75.7%; Score 84; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETHKPCCAPT 14
 :|||||
 Db 21 INPETHKPCCAPT 34

RESULT 11
 A43918
 TGF-beta-related protein 60A precursor - fruit fly (Drosophila melanogaster)
 N/Alternate names: bone morphogenetic protein homolog precursor
 C/Species: Drosophila melanogaster
 C/Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C/Accession: A43918; A41233
 R/Doctor, J.S.; Jackson, P.D.; Raehka, K.E.; Vissalli, M.; Hoffmann, F.M.
 Dev. Biol. 151, 491-505, 1992
 A>Title: Sequence, biochemical characterization, and developmental expression of a new m
 A/Reference number: A43918; MUID:92290120; PMID:1601181
 A/Accession: A43918
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-455 <DOC>
 A/Cross-references: GB:M84795; NID:g156729; PIDN:AAA28307.1; PID:g156730
 A/Note: sequence extracted from NCBI backbone (NCBIN:106399, NCBI:P:106400)
 R/Marton, K.A.; Thomsen, G.H.; Gelbart, W.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 9214-9218, 1991
 A>Title: Drosophila 60A gene, another transforming growth factor beta family member, is
 A/Reference number: A41233; MUID:92021021; PMID:1524384
 A/Accession: A41233
 A/Molecule type: mRNA
 A/Residues: 1-455 <WMA>
 A/Cross-references: GB:M77012; NID:g156727; PIDN:AAA28306.1; PID:g156728
 C/Comment: This protein is a member of the transforming growth factor beta family.
 C/Genetics:
 A/Gene: 60A
 A/Cross-references: FlyBase:FBgn0024234

C:Superfamily: inhibin
C:Keywords: homodimer

Query Match 69.4%; Score 77; DB 2; Length 455;
Best Local Similarity 63.2%; Pred. No. 0.0012;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPPTOLNAIS 19
DB 410 LEPKVPKPCCAPPTOLGAL 428

RESULT 12

A29619
Vgl embryonic growth factor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 21-Jul-2000
C:Accession: A29619
R:Weeks, D.L.; Melton, D.A.
Cell 51, 861-867, 1987

A:Title: A maternal mRNA localized to the vegetal hemisphere in Xenopus eggs codes for a
A:Reference number: A29619; MUID:88052889; PMID:3479264

A:Accession: A29619
A:Molecule type: mRNA
A:Residues: 1-360 <WEB>
A:Cross-references: GB:M18055; NID:g214179; PIDN:AAA49727.1; PID:g214180
C:Superfamily: inhibin
C:Keywords: growth factor

Query Match 64.0%; Score 71; DB 2; Length 360;
Best Local Similarity 55.0%; Pred. No. 0.0074;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPPTOLNAIS 20
DB 315 IEPEDIPKPCCVPTKMSPTIS 334

RESULT 13

A26158
decentuplegic protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C>Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999
C:Accession: A26158
R:Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.
Nature 325, 81-84, 1987

A:Title: A transcript from a Drosophila pattern gene predicts a protein homologous to th
A:Reference number: A26158; MUID:87090408; PMID:3467201

A:Accession: A26158
A:Molecule type: mRNA
A:Residues: 1-588 <PAD>
A:Cross-references: GB:M30116; NID:g157291; PID:g157292
C:Genetics:

A:Gene: FlyBase:dpp
A:Cross-references: FlyBase:Fgn0000490
C:Keywords: glycoprotein
F/1-15/Domain: signal sequence #status predicted <SIG>
F/120,342,377,529/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 71; DB 2; Length 588;
Best Local Similarity 55.0%; Pred. No. 0.012;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPPTOLNAIS 20
DB 543 MNPGRVPRKACVPTOLDIVA 562

RESULT 14

A45056

osteogenic protein 2 precursor - human
N/Alternate names: bone morphogenetic protein 8; OP-2
C:Species: Homo sapiens (man)

C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A45056
R:Ozkeynak, E.; Schlegelberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier, E.

J. Biol. Chem. 267, 25230-25237, 1992
A:Title: Osteogenic protein-2. A new member of the transforming growth factor-beta super
A:Reference number: A45056; MUID:93094231; PMID:1460021

A:Accession: A45056
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-402 <OZK>

A:Cross-references: GB:M97016; NID:g189389; PIDN:AB01360.1; PID:g189390
A:Experimental source: hippocampus
A>Note: sequence extracted from NCBI backbone (NCBIP:120189)

A:Gene: GDB:BMP8; OP-2
A:Cross-references: GDB:136392
C:Superfamily: inhibin

Query Match 63.1%; Score 70; DB 2; Length 402;
Best Local Similarity 60.0%; Pred. No. 0.011;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPPTOLNAIS 20
DB 357 MKNVAVPRKACAPTKLSATS 376

RESULT 15

S52408
SPDVR1 protein - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)
C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
C:Accession: S52408
R:Ponce, M.R.; Micol, J.L.; Davidson, E.H.
Submitted to the EMBL Data Library, February 1995

A:Description: SPDVR1, a member of the transforming growth factor-beta superfamily expres
A:Reference number: S52408
A:Accession: S52408
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-461 <PON>

A:Cross-references: EMBL:Z48313; NID:g673496; PID:g673497
C:Superfamily: inhibin

Query Match 63.1%; Score 70; DB 2; Length 461;
Best Local Similarity 55.0%; Pred. No. 0.013;
Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 INPETHKPCCAPPTOLNAIS 20
DB 416 MSPSHVPRKPCAPTKLSPTIT 435

Search completed: October 12, 2004, 09:38:16
Job time : 31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2004, 09:02:13 ; Search time 89 Seconds
(without alignments)
70.903 Million cell updates/sec

Title: US-10-619-910-11

Perfect score: 111

Sequence: 1 INPRTVPRKPCAPDTOLNAIS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	100.0	49	6 Q9MZL9	Q9MZL9 canis faml
2	111	100.0	108	6 Q8WTCO	Q8WTCO oviss aries
3	111	100.0	313	13 Q91403	Q91403 gallus gall
4	111	100.0	398	13 Q91876	Q91876 gallus gall
5	108	97.3	141	11 Q88684	Q88684 rattus norv
6	108	97.3	306	11 Q9R228	Q9R228 rattus norv
7	108	97.3	424	13 Q9YGH7	Q9YGH7 xenopus lae
8	102	91.9	432	13 Q9PTP9	Q9PTP9 brachydanio
9	97	87.4	100	6 Q8WTC1	Q8WTC1 oviss aries
10	97	87.4	435	11 Q8BRM3	Q8BRM3 mus musculu
11	97	87.4	506	11 Q811S4	Q811S4 rattus norv
12	89	80.2	446	13 Q71288	Q71288 brachydanio
13	87	78.4	453	13 P87373	P87373 gallus gall
14	87	78.4	454	11 Q8CCE0	Q8CCE0 mus musculu
15	79	71.2	87	5 Q9UNG4	Q9UNG4 halicoris tu
16	79	71.2	178	5 Q25211	Q25211 junonia coe

17	78	70.3	204	5 Q9XZ69	Q9XZ69 triptenes
18	78	70.3	289	5 Q9XQ08	Q9XQ08 strongyloce
19	78	70.3	417	5 Q9XQ07	Q9XQ07 lytechinus
20	77	69.4	461	5 Q8MX23	Q8MX23 hemiceutrus
21	76	68.5	77	5 Q8WR85	Q8WR85 antedon bif
22	75	67.6	301	5 Q97390	Q97390 crassostrea
23	74	66.7	128	5 Q95W38	Q95W38 schistocerc
24	74	66.7	354	13 Q9YGV1	Q9YGV1 xenopus lae
25	74	66.7	614	5 P91720	P91720 drosophila
26	73	65.8	191	5 Q26468	Q26468 schistocerc
27	72	64.9	412	11 Q80VZ0	Q80VZ0 mus musculu
28	72	64.9	438	5 Q9GT26	Q9GT26 anopheles s
29	71	64.0	356	13 Q712G5	Q712G5 xenopus bor
30	71	64.0	399	11 Q8BNC2	Q8BNC2 mus musculu
31	71	64.0	588	5 Q9VOC6	Q9VOC6 drosophila
32	70	63.1	361	5 Q96504	Q96504 brachyisto
33	70	63.1	378	5 Q8MXC2	Q8MXC2 acropora mi
34	70	63.1	402	4 Q725T6	Q725T6 homo sapien
35	70	63.1	411	5 Q9U4I8	Q9U4I8 brachyisto
36	70	63.1	443	5 Q76851	Q76851 halocynthia
37	68.5	61.7	398	13 Q90YD7	Q90YD7 xenopus tro
38	68	61.3	370	5 Q869A4	Q869A4 acaearanea
39	68	61.3	407	5 Q8MGC4	Q8MGC4 patella vul
40	67	60.4	509	5 Q8MS99	Q8MS99 archaeter c
41	66	59.5	85	5 Q8BHW7	Q8BHW7 paracentrot
42	66	59.5	301	5 Q86RL7	Q86RL7 llyanassa o
43	66	59.5	373	13 Q98950	Q98950 gallus gall
44	66	59.5	373	13 Q90723	Q90723 gallus gall
45	65	58.6	83	13 P79707	P79707 cynops pyrr

ALIGNMENTS

RESULT 1

Q9MZL9 PRELIMINARY; PRT; 49 AA.

AC Q9MZL9 01-OCT-2000 (TRENBLREL.15, Created)
 DT 01-OCT-2000 (TRENBLREL.15, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL.22, Last annotation update)
 DE Bone morphogenetic protein BMP7 (Fragment).
 OS Canis familiaris (Dog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Johanson J.A., Breen M., Murphy K.E.;
 RT "Chromosomal Localization of the Genes Encoding Canine Bone
 RT Morphogenetic Proteins 4 and 7 (BMP4 and BMP7).";
 RL Submitted (UTL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF172412; AAFB9752.1; -.
 DR HSSP; P18075; BMP.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 FT NON_TER
 FT
 SQ SEQUENCE 49 AA; 5493 MW; 9AF2C1B144E26EFB CRC64;

Query Match 100.0%; Score 111; DB 6; Length 49;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

Q8WTCO 1 INPRTVPRKPCAPDTOLNAIS 20
 Db 4 INPRTVPRKPCAPDTOLNAIS 23

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ID 08MUC0 PRELIMINARY; PRT; 108 AA.
AC 08MUC0;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Bone morphogenetic protein 7 (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Souza C.J.H., Baird D.T.;
RT "BMP expression in the sheep ovary.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF508311; AAM46923.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-protetide; 1.
DR PRINTS; PR00438; GFCYSKNOT.

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DR PRINTS; PR00669; INHIBINA.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
FT NON TER 1
SC SEQUENCE 313 AA; 35816 MW; C0A3739197DEAC8F CRC64;

```

```

Query Match 100.0%; Score 111; DB 13; Length 313;
Best Local Similarity 100.0%; Pred. No. 6,3e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 INPETYKPCCAPTOLNAIS 20
268 INPETYKPCCAPTOLNAIS 287

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RESULT 4

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ID 0918T6 PRELIMINARY; PRT; 398 AA.
AC 0918T6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Bone morphogenetic protein 7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE:Oviduct;
RC MEDLINE=20307867; PubMed=10848589;
RX Monroe D.G., Jin D.F., Sanders M.M.;
RT "Bistrogen Opposes the Apoptotic Effects of Bone Morphogenetic Protein
RT 7 on Tissue Remodeling.";
RL Mol. Cell. Biol. 20:4626-4634(2000).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF205877; AAF34179.1; -.
DR HSSP; P18075; BMP.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb-protetide; 1.
DR PRINTS; PR00669; INHIBINA.
DR PRODOM; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
DR NON TER 1
SC SEQUENCE 398 AA; 45459 MW; 9C3F62529DDC37 CRC64;

```

```

Query Match 100.0%; Score 111; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 2,2e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Db 1 INPETYKPCCAPTOLNAIS 20
85 INPETYKPCCAPTOLNAIS 104

```

RESULT 3

```

ID 091403 PRELIMINARY; PRT; 313 AA.
AC 091403;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Bone morphogenetic protein-7 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95200473; PubMed=7893347;
RA Houston B., Thorp B.H., Butte D.W.;
RT "Molecular cloning and expression of bone morphogenetic protein-7 in
RT the chick epiphyseal growth plate.";
RL J. Mol. Endocrinol. 13:289-301(1994).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; S77477; AAB3846.1; -.
DR PIR; I51284; I51284.
DR HSSP; P18075; BMP.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb-protetide; 1.
DR PRINTS; PR00438; GFCYSKNOT.

```

```

Query Match 100.0%; Score 111; DB 13; Length 398;
Best Local Similarity 100.0%; Pred. No. 8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 1 INPETYKPCCAPTOLNAIS 20
353 INPETYKPCCAPTOLNAIS 372

```

RESULT 5

```

ID 088684 PRELIMINARY; PRT; 141 AA.
AC 088684;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Bone morphogenetic protein-7 (Fragment).
OS Rattus norvegicus (Rat).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar;
RX MEDLINE=97107792; PubMed=8950518;
RA Takahashi H., Ikeda T.;
RT "Transcripts for two members of the transforming growth factor-beta
superfamily BMP-3 and BMP-7 are expressed in developing rat embryos."
RL Dev. Dyn. 207:439-449(1996).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; D29769; BAA31853.1; -
DR HSSP; P18075; IAMP.
DR GO; GO:0005576; C:extracellular; IEA.
DR CO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR002405; Inhibin_alpha.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
FT NON_TER 1
FT 141 141
SQ SEQUENCE 141 AA; 15850 MW; 1A02FA213F39812 CRC64;

Query Match 97.3%; Score 108; DB 11; Length 141;
Best Local Similarity 95.0%; Pred. No. 8.7e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETHPCCAPPTOLNAIS 20
Db 110 INPETHPCCAPPTOLNAIS 129

RESULT 6
Q9R228 PRELIMINARY; PRT; 306 AA.
AC Q9R228;
ID 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Bone morphogenetic protein 7 precursor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney;
RX MEDLINE=99170602; PubMed=10070161;
RA Simon M., Mareah J.G., Harris S.E., Hernandez J.D., Arar M.,
RA Olson M.S., Abboud H.E.;
RT "Expression of bone morphogenetic protein-7 mRNA in normal and
ischemic adult rat kidney."
RL Am. J. Physiol. 276:F382-F389(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF100787; AAD27804.1; -
DR HSSP; P18075; IAMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
FT NON_TER 1
FT 306 306
SQ SEQUENCE 306 AA; 34953 MW; BB53FC5E9592400 CRC64;

Query Match 97.3%; Score 108; DB 11; Length 306;
Best Local Similarity 95.0%; Pred. No. 1.9e-09;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 INPETHPCCAPPTOLNAIS 20
Db 274 INPETHPCCAPPTOLNAIS 293

RESULT 7
Q9YGH7 PRELIMINARY; PRT; 424 AA.
AC Q9YGH7;
ID 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Osteogenic protein-1 homolog precursor (Hypothetical protein).
GN XOP-1H.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang S., Krinks M., Kleinwaks L., Zapalo P., Moos M. Jr.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Helel F.,
RA Datchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Casarini P., Prange C.,
RA Bosa S.S., Ioduciano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Roark S.A., McMan P.J., McKernan K.J., Malek J.A., Gunatirane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huij S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalins D.E., Schmechel A., Schein J.E.,
RA Jones S.U., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
cDNA and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; U40034; AAD09399.1; -
DR EMBL; BC059599; AAH59599.1; -
DR HSSP; P18075; IAMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Hypothetical protein; signal. POTENTIAL.
 FT SIGNAL 286 424 OSTEOGENIC PROTEIN-1 HOMOLOG.
 FT CHAIN 424 AA; 48917 MW; C4638CDDSD0AIDE4 CRC64;
 SQ SEQUENCE

Query Match 97.3%; Score 108; DB 13; Length 424;
 Best Local Similarity 95.0%; Pred. No. 2.6e-09;
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPEYVPCPCAPTQNLNLS 20
 DB 379 INPEYVPCPCAPTQNLNLS 398

RESULT 8
 Q8PPT9 PRELIMINARY; PRT; 432 AA.
 ID Q8PPT9
 AC Q8PPT9; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Bone morphogenetic protein 7.
 GN BMP7 OR BMP7.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TL;
 RA Dick A., Hild M., Bauer H., Imai Y., Maifeld H., Schier A.F.,
 RA Talbot M.S., Bouwmeester T., Hamerschmidt M.,
 RT "Essential role of BMP7 (snailhouse) and its prodomain in dorsoventral
 RT patterning of the zebrafish embryo.";
 RL Development 0:0-0(2000).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF201379; AAF17558.1; -.
 DR HSSP; F18075; 1BMP.
 DR ZFIN; ZDB-GENE-000208-25; bmp7.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00668; TGFb propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE 432 AA; 48923 MW; C982AP80E1652156 CRC64;

Query Match 91.9%; Score 102; DB 13; Length 432;
 Best Local Similarity 90.0%; Pred. No. 2.6e-08;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPEYVPCPCAPTQNLNLS 20
 DB 387 INPEYVPCPCAPTQNLNLS 406

RESULT 9
 Q8MUC1 PRELIMINARY; PRT; 100 AA.
 ID Q8MUC1
 AC Q8MUC1; 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Bone morphogenetic protein 6 (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxId=9940;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Souza C.J.H., Baird D.T.;
 RT "BMP expression in the sheep ovary.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF508310; AAM46922.1; -.
 DR GO; GO:000576; Cytoskeletal; IEA.
 DR GO; GO:0008151; P; cell growth and/or maintenance; IEA.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 FT NON_TER 1
 FT NON_TER 100
 SQ SEQUENCE 100 AA; 11309 MW; 8CB61551F356350 CRC64;

Query Match 87.4%; Score 97; DB 6; Length 100;
 Best Local Similarity 85.0%; Pred. No. 3.8e-08;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPEYVPCPCAPTQNLNLS 20
 DB 67 MNPEYVPCPCAPTQNLNLS 86

RESULT 10
 Q8BRW3 PRELIMINARY; PRT; 435 AA.
 ID Q8BRW3
 AC Q8BRW3; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Bone morphogenetic protein 6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Artery, and Vein;
 RC STRAIN=C57BL/6J; TISSUE=Artery, and Vein;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK041210; BAC30864.1; -.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00668; TGFb propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE 435 AA; 48438 MW; E26CFE2180E20F76 CRC64;

Query Match 87.4%; Score 97; DB 11; Length 435;
 Best Local Similarity 85.0%; Pred. No. 1.7e-07;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPEYVPCPCAPTQNLNLS 20
 DB 390 MNPEYVPCPCAPTQNLNLS 409

RESULT 11
 Q811S4 PRELIMINARY; PRT; 506 AA.
 ID Q811S4
 AC Q811S4; 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Bone morphogenetic protein 6.
 GN BMP6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley;
 RA Li H., Li Y., Piltman D.D., Amalfitano A., Hankins G.R., Helm G.A.;
 RT "An Immunological Study of BMP6 Adenoviral Gene Therapy."
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY184240; AAC25744.1; -
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE 506 AA; 56222 MW; 703D077D7E94416C CRC64;

Query Match 87.4%; Score 97; DB 11; Length 506;
 Best Local Similarity 85.0%; Pred. No. 2e-07;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INPEYKPCCAPTQNAIS 20
 Db 461 MNPEYKPCCAPTKNAIS 480

RESULT 12
 ID 071288 PRELIMINARY; PRT; 446 AA.
 AC 071288;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RN NCBI_TaxID=7955;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein W.C., Usdin T.B., Ioshizuka S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;

RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC054647; AAB54647.1; -
 GN Hypothetical protein.
 OS KM
 SQ SEQUENCE 446 AA; 50519 MW; D2C2021089570F84 CRC64;

Query Match 80.2%; Score 89; DB 13; Length 446;
 Best Local Similarity 83.3%; Pred. No. 3.5e-06;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PETVPRPCCAPTQNAIS 20
 Db 403 PDNVKPRPCCAPTKNAIS 420

RESULT 13
 ID P87373 PRELIMINARY; PRT; 453 AA.
 AC P87373;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
 DE BMP5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN NCBI_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97000882; PubMed=8815925;
 RA Oh S.H., Johnson R., Wu D.K.;
 RT "Differential expression of bone morphogenetic proteins in the
 developing vestibular and auditory sensory organs";
 RL J. Neurosci. 16:6463-6475(1996).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; S83278; AAB49514.1; -
 DR HSSP; P18075; BMP.
 DR InterPro; IPR002400; GF_cysknob.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE 453 AA; 51628 MW; AB946FB878BF32B2 CRC64;

Query Match 78.4%; Score 87; DB 13; Length 453;
 Best Local Similarity 83.3%; Pred. No. 7.5e-06;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PETVPRPCCAPTQNAIS 20
 Db 410 PDNVKPRPCCAPTKNAIS 427

RESULT 14
 ID 08CC60 PRELIMINARY; PRT; 454 AA.
 AC 08CC60;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
 DE Bone morphogenetic protein 5.
 GN BMP5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RP [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; Tissue=Lung;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL: AK033862; BAC28247.1; -.
 DR MGD: MG1:88181; Bmp5.
 DR GO: GO:0007389; P:pattern specification; IMP.
 DR GO: GO:0001501; P:skeletal development; IMP.
 DR InterPro: IPR002400; Gf_cysknot.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF000688; TGF_beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE 454 AA; 51727 MW; 722EA34FF25D63A0 CRC64;

Search completed: October 12, 2004, 09:37:40
 Job time : 91 secs

Query Match 78.4%; Score 87; DB 11; Length 454;
 Best Local Similarity 83.3%; Pred.No. 7.5e-06;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 PETVPRKCCAPTOLNAIS 20
 | : ||||| : |||||
 Db 411 PDHVPKCCAPTOLNAIS 428

RESULT 15
 Q9UIG4 PRELIMINARY; PRT; 87 AA.
 ID O9UIG4;
 AC O9UIG4;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)
 DE BMP2/4 protein (Fragment).
 GN BMP2/4.
 OS Halictis tuberculata.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Vetigastropoda; Halictoidae; Halictidae; Halictis.
 OX NCBI_TaxID=96103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Mantle;
 RX MEDLINE=21261484; PubMed=11368850;
 RA Jelong C, Mathieu M, Favrel P;
 RT "Identification of new bone morphogenetic protein-related members in
 RT invertebrates.";
 RL Biochimie 83:423-426(2001).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AJ251823; CAB63656.1; -.
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF000688; TGF_beta; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 FT NON_TER 1
 FT NON_TER 87
 SQ SEQUENCE 87 AA; 9565 MW; 705965FCHDEFF6 CRC64;

Query Match 71.2%; Score 79; DB 5; Length 87;
 Best Local Similarity 65.0%; Pred.No. 2.9e-05;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 INPETVPRKCCAPTOLNAIS 20
 : ||||| : |||||
 Db 44 VNPSAVPRKCCAPTOLNAIS 63

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OM protein - protein search, using sw model

Run on: October 12, 2004, 09:02:13 ; Search time 19 Seconds

(without alignments)
54.811 Million cell updates/sec

Title: US-10-619-910-11

Perfect score: 111

Sequence: 1 IMPETVPPKCCAPQLNALS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	111	100.0	431	1	BMP7_HUMAN
2	108	97.3	430	1	BMP7_MOUSE
3	107	96.4	426	1	BMP7_XENLA
4	97	87.4	207	1	BMP6_RAT
5	97	87.4	510	1	BMP6_MOUSE
6	97	87.4	513	1	BMP6_HUMAN
7	87	78.4	452	1	BMP5_MOUSE
8	87	78.4	454	1	BMP5_HUMAN
9	77	69.4	436	1	60A_DROVI
10	77	69.4	435	1	60A_DROME
11	72	64.9	399	1	BMP8_MOUSE
12	72	64.9	321	1	DECA_DROPS
13	71	64.0	360	1	DVRI_XENLA
14	71	64.0	399	1	BMP8_MOUSE
15	71	64.0	588	1	DECA_DROME
16	71	64.0	593	1	DECA_DROST
17	70	63.1	402	1	BMP8_HUMAN
18	70	63.1	461	1	DVRI_STRPU
19	67	60.4	372	1	DECA_TRICA
20	65	58.6	395	1	UNIV_STRPU
21	65	57.7	401	1	BMP4_XENLA
22	64	57.7	405	1	BMP4_CHICK
23	64	57.7	408	1	BMP4_DANDA
24	64	57.7	408	1	BMP4_HUMAN
25	64	57.7	408	1	BMP4_MOUSE
26	64	57.7	408	1	BMP4_RAT
27	64	57.7	409	1	BMP4_RABIT
28	64	57.7	427	1	DSLI_CHICK
29	63	56.8	308	1	GDPE_HUMAN
30	63	56.8	353	1	BMP2_HUMAN
31	63	56.8	393	1	BMP2_CHICK
32	63	56.8	394	1	BMP2_RAT
33	63	56.8	395	1	BMP2_MOUSE
					BMP2_RABIT
					O46564 oryctolagus

34	63	56.8	396	1	BMP2_DANDA	O19006 dama dama (
35	63	56.8	396	1	BMP2_HUMAN	P12643 homo sapien
36	63	56.8	398	1	BMP4_XENLA	P30884 xenopus lae
37	63	56.8	398	1	BMP8_XENLA	P30884 xenopus lae
38	63	56.8	495	1	GDPE_MOUSE	P43027 mus musculu
39	63	56.8	501	1	GDPE_HUMAN	P43028 homo sapien
40	61	55.0	400	1	SCW_DROME	P54631 drosophila
41	59	53.2	355	1	DVRI_BRARE	P35621 brachydario
42	55	49.5	125	1	GDPE_MOUSE	P43028 mus musculu
43	55	49.5	436	1	GDPE_BOVIN	P5106 bos taurus
44	54	48.6	303	1	GDPE_MOUSE	Q92037 mus musculu
45	54	48.6	303	1	GDPE_RAT	Q92036 rattus norv

ALIGNMENTS

RESULT 1
BMP7_HUMAN STANDARD; PRT; 431 AA.
AC P18075; Q9H512; Q9T07.
DI 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DR 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bone morphogenetic protein 7 precursor (BMP-7) (osteogenic protein 1)
DE (OP-1).
CN BMP7 OR OP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=90291971; PubMed=2357959;
RA Oezkeynak E., Rueger D.C., Drier E.A., Corbett C., Ridge R.J.,
RT Sampath T.K., Oppermann H.,
RL "OP-1 cDNA encodes an osteogenic protein in the TGF-beta family.";
RN EMBO J. 9:2085-2093(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9108608; PubMed=2263636;
RA Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA Wang E.A., Wozney J.M.,
RA "Identification of transforming growth factor beta family members
RT present in bone-inductive protein purified from bovine bone.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Garder C., Carter N.P.,
RA Chapman U.C., Clamp W., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cobby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Griffiths D.V., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehevaeslath M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., Murray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Rose M.T., Scott C.B., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith W.L., Soderlund C., Steward C.A., Sulston C.E.,
RA Swann R.M., Symcote N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitlaker P., Willey D.L., Williams L., Williams S.A.,

RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyx S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (5)
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 293-431.
 RX MEDLINE=96149402; PubMed=8570652;
 RA Griffith D.L., Keck P.C., Sampath T.K., Rueger D.C., Carlson W.D.;
 RT "Three-dimensional structure of recombinant human osteogenic protein
 RT 1: structural paradigm for the transforming growth factor beta
 RT superfamily.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:878-883(1996).
 CC - FUNCTION: Induces cartilage and bone formation. May be the
 CC osteoinductive factor responsible for the phenomenon of epithelial
 CC osteogenesis. Plays a role in calcium regulation and bone
 CC homeostasis.
 CC - SUBUNIT: Homodimer; disulfide-linked.
 CC - TISSUE SPECIFICITY: EXPRESSED IN THE KIDNEYS AND BLADDER. LOWER
 CC LEVELS SEEN IN THE BRAIN.
 CC - SIMILARITY: Belongs to the TGF-beta family.
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 CC -----
 DR EMBL: X51801; CAA36100.1; -
 DR EMBL: M60316; AAA36738.1; -
 DR EMBL: AL122058; CAB90273.1; -
 DR EMBL: AL157414; CAC08434.1; -
 DR EMBL: BC006584; AAH08584.1; -
 DR PIR: C39263; EKHU7.
 DR PDB: 1BMP; 23-JUL-97.
 DR PDB: 1MAU; 18-DEC-02.
 DR GeneW: HGNC:1074; BMP7.
 DR MIM: 112267; -
 DR GO: GO:0001501; P:skeletal development; TAS.
 DR InterPro: IPR001839; TGFp.
 DR InterPro: IPR001111; TGFp.N.
 DR Pfam: PF000688; TGFp_beta; 1.
 DR Pfam: PF000688; TGFp_propeptide; 1.
 DR ProDom: PD000357; TGFp; 1.
 DR SMART: SM00204; TGFp; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Signal: Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW Glycoprotein; 3d-structure.

FT SIGNAL 1 29
 FT PROPEP 30 292
 FT CHAIN 293 431
 FT DISULFID 330 396
 FT DISULFID 359 428
 FT DISULFID 363 430
 FT DISULFID 395 395
 FT CARBOHYD 187 187
 FT CARBOHYD 302 302
 FT CARBOHYD 321 321
 FT CARBOHYD 372 372
 FT STRAND 329 329
 FT STRAND 331 333
 FT STRAND 336 342
 FT HELIX 339 348
 FT TURN 343 347
 FT TURN 348 350
 FT STRAND 353 355
 FT STRAND 358 360
 FT STRAND 362 362
 FT TURN 370 371
 FT TURN 375 386
 FT HELIX 388 390
 FT STRAND 396 409
 FT STRAND 411 413
 FT HELIX 415 431
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 SO SEQUENCE 431 AA; 49313 MW; 47A05E45C6815F8A CRC64;
 Query Match 100.0%; Score 111; DB 1; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.9e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 INBETWPKPCAPTOLNATS 20
 DB 386 INBETWPKPCAPTOLNATS 405
 RESULT 2
 ID BMP7_MOUSE STANDARD; PRT; 430 AA.
 AC P23359; 091XF7;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 7 precursor (BMP-7) (Osteogenic protein 1)
 DE (OP-1).
 GN BMP7 OR BMP-7 OR OP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91354237; PubMed=1715687;
 RA Oezkaynak E., Schmiegelsberg P.N.J.; Oppermann H.;
 RT "Mxrtine osteogenic protein (OP-1): high levels of mRNA in kidney.";
 RL Biochem. Biophys. Res. Commun. 179:116-123(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyx S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Induces cartilage and bone formation. May be the
CC osteoinductive factor responsible for the phenomenon of epithelial
CC osteogenesis. Plays a role in calcium regulation and bone
CC homeostasis.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X56906; CAA40222.1; -
CC EMBL: BC010771; AAH10771.1; -
CC HSSP: P18075; IBM.
CC MGD: MGI:103302; Bmp7.
CC GO: GO:0005615; Extracellular space; IDA.
CC GO: GO:0005515; Fibrinogen binding; IPI.
CC GO: GO:0007411; Paxon guidance; IDA.
CC GO: GO:0009887; Proliferation; IMP.
CC GO: GO:0007389; Proliferation; IMP.
CC GO: GO:0007435; Proliferation; IMP.
CC InterPro: IPR001839; TGF-beta.
CC InterPro: IPR001111; TGF-beta.
CC Pfam: PF00019; TGF-beta; 1.
CC ProDom: PD000357; TGF-beta; 1.
CC SMART: SMO0204; TGF-beta; 1.
CC PROSITE: PS00250; TGF-beta; 1.
CC Signal: Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
CC Glycoprotein.
CC KMW SIGNAL 1 29
CC PROPEP 291
CC FT CHAIN 292 430 BONE MORPHOGENETIC PROTEIN 7.
CC FT DISULFID 329 395 BY SIMILARITY.
CC FT DISULFID 358 427 BY SIMILARITY.
CC FT DISULFID 362 429 BY SIMILARITY.
CC FT DISULFID 394 394 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 167 167 A -> R (IN REF. 1).
CC SEQUENCE 430 AA; 49198 MM; 4645365D2E54041 CRC64;
Query Match 97.3%; Score 108; DB 1; Length 430;
Best Local Similarity 95.0%; Pred. No. 8e-09;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 INPETYKPCCAPTQNAIS 20
DB 385 INPDVPRKPCAPTQNAIS 404
RESULT 3
BMP7_XENLA STANDARD; PRT; 426 AA.
AC P30866; Q91645;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Bone morphogenetic protein 7 precursor (BMP-7) (Osteogenic protein 1)

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DE (Op-1) (Xenopus).
GN BMP7.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RX MEDLINE=92378616; PubMed=1510675;
RA Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RT "Genes for bone morphogenetic proteins are differentially transcribed
RT in early amphibian embryos."
RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
RL [2]
RP SEQUENCE FROM N.A.
RP Hawley S.H.B., Wunnenberg-Stapleton K., Hashimoto C.,
RP Laurent M.N., Mathe T., Blumberg B.W., Cho K.W.Y.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Induces cartilage and bone formation. May be the
CC osteoinductive factor responsible for the phenomenon of epithelial
CC osteogenesis. Plays a role in calcium regulation and bone
CC homeostasis.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X63427; CAA45021.1; -
CC EMBL: U38559; AA82616.1; -
CC PIR: JH0690; JH0690.
CC HSSP: P18075; IBM.
CC InterPro: IPR001839; TGF-beta.
CC InterPro: IPR001111; TGF-beta.
CC Pfam: PF00019; TGF-beta; 1.
CC ProDom: PD000357; TGF-beta; 1.
CC SMART: SMO0204; TGF-beta; 1.
CC PROSITE: PS00250; TGF-beta; 1.
CC Signal: Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
CC Glycoprotein.
CC KMW SIGNAL 1 22
CC PROPEP 282
CC FT CHAIN 283 426 BONE MORPHOGENETIC PROTEIN 7.
CC FT DISULFID 325 391 BY SIMILARITY.
CC FT DISULFID 354 423 BY SIMILARITY.
CC FT DISULFID 358 425 BY SIMILARITY.
CC FT DISULFID 390 390 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 317 319 KRR -> NVV (IN REF. 2).
CC CONFLICT 355 355 D -> E (IN REF. 2).
CC SEQUENCE 426 AA; 48965 MM; 6401D51AC97117 CRC64;
Query Match 96.4%; Score 107; DB 1; Length 426;
Best Local Similarity 95.0%; Pred. No. 1.1e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 INPETYKPCCAPTQNAIS 20
DB 381 INPDVPRKPCAPTQNAIS 400
RESULT 4
BMP6_RAT STANDARD; PRT; 207 AA.
ID BMP6_RAT

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FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 73 73 K -> M (IN REF. 3).
 FT CONFLICT 75 75 E -> K (IN REF. 3).
 FT CONFLICT 86 86 L -> P (IN REF. 3).
 SQ SEQUENCE 510 AA; 56431 MW; 910868531289FCD2 CRC64;
 Query Match 87.4%; Score 97; DB 1; Length 510;
 Best Local Similarity 85.0%; Pred. No. 4,2e-07;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPETYPCPCAPTQNAIS 20
 DB 465 MNPEYVPCPCAPTQNAIS 484
 RESULT 6
 BNP6_HUMAN STANDARD; PRT; 513 AA.
 ID BNP6_HUMAN
 AC P22004;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 6 precursor (BMP-6).
 GN BMP6 OR VGR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=bone;
 RA MEDLINE=91086808; PubMed=2263636;
 RA Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
 Wang E.A., Wozney J.M.;
 RT Identification of transforming growth factor beta family members
 present in bone-inductive protein purified from bovine bone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
 CC -1- FUNCTION: Induces cartilage and bone formation.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
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 CC -----
 CC EMBL: M60315; AAA36737.1; -
 CC PIR: B39263; BMHUS.
 CC HSP: P18075; IBMF.
 CC HSP: P18075; IBMF.
 DR HSP: P18075; IBMF.
 DR GO: GO:0001501; P:skeletal development; TAS.
 DR GO: GO:112266; -
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb N.
 DR Pfam: PF00019; TGF-beta; I.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW Glycoprotein.
 FT SIGNAL 1 20
 FT PROPEP 21 361
 FT CHAIN 362 513 BONE MORPHOGENETIC PROTEIN 6.
 FT DISULFID 412 478 BY SIMILARITY.
 FT DISULFID 441 478 BY SIMILARITY.
 FT DISULFID 445 512 BY SIMILARITY.
 FT DISULFID 477 477 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 513 AA; 57225 MW; 3F19155B36049278 CRC64;
 Query Match 87.4%; Score 97; DB 1; Length 513;
 Best Local Similarity 85.0%; Pred. No. 4,2e-07;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPETYPCPCAPTQNAIS 20
 DB 468 MNPEYVPCPCAPTQNAIS 487
 RESULT 7
 BNP5_MOUSE STANDARD; PRT; 452 AA.
 ID BNP5_MOUSE
 AC P49003;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 5 precursor (BMP-5).
 GN BMP5 OR Bmp-5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/KW;
 RA MEDLINE=95046894; PubMed=7958439;
 RA King J.A., Marker P.C., Seung K.J., Kingsley D.M.;
 RT "BMP5 and the molecular, skeletal, and soft-tissue alterations in
 short ear mice.";
 RL Dev. Biol. 166:112-122(1994).
 CC -1- FUNCTION: Induces cartilage and bone formation.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
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 CC -----
 CC EMBL: L41145; AAA64612.1; -
 CC PIR: I49542; I48542.
 CC HSP: P18075; IBMF.
 CC HSP: P18075; IBMF.
 DR HSP: P18075; IBMF.
 DR GO: GO:0007389; P:pattern specification; IMP.
 DR GO: GO:0001501; P:skeletal development; IMP.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb N.
 DR Pfam: PF00019; TGF-beta; I.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW Glycoprotein.
 FT SIGNAL 1 25
 FT PROPEP 26 320
 FT CHAIN 321 452 BONE MORPHOGENETIC PROTEIN 5.
 FT DISULFID 351 417 BY SIMILARITY.
 FT DISULFID 380 449 BY SIMILARITY.
 FT DISULFID 384 451 BY SIMILARITY.
 FT DISULFID 416 416 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 452 AA, 51511 MW, AAD9521BC94A78D5 CRC64;
 Query Match 78.4%; Score 87; DB 1; Length 452;
 Best Local Similarity 83.3%; Pred. No. 1,2e-05;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 PETVPRKPCCAPTQNLNALS 20
 DB 409 PDHVPKPCCAPTQNLNALS 426
 RESULT 8
 ID B_MPS_HUMAN STANDARD; PRT; 454 AA.
 AC P22003; Q9H547; Q9NTM5;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 5 precursor (BMP-5).
 GN BMP5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=91088608; PubMed=2263636;
 RA Celeste A.O., Iannuzzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
 Wang E.A., Wozney J.M.;
 RT Identification of transforming growth factor beta family members
 RT present in bone-inductive protein purified from bovine bone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bates K., Tracey A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultix S.W.,
 Villalon D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fehey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schwartz J., Myers R.M.,
 Butlerfield Y.S.N., Krzyzinski M.T., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra N.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Induces cartilage and bone formation.
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in the lung and liver.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
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 CC -----
 DR EMBL; M60314; AAA6736.1; -;
 DR EMBL; AL137178; CAC12765.1; -;
 DR EMBL; AL133586; CAB81657.1; -;
 DR EMBL; BC027958; AAB27958.1; -;
 DR PIR; A39263; BMTU5.
 DR HSSP; P18075; 1BMP.
 DR Genem; HGNC:1072; BMP5.
 DR MIM; 112655; -;
 DR GO; GO:0005125; Fc cytokine activity; NAS.
 DR GO; GO:0001501; P: skeletal development; NAS.
 DR InterPro; IPR002400; GF_cys_knot.
 DR InterPro; IPR001839; TGF_beta.
 DR InterPro; IPR001111; TGF_beta.
 DR Pfam; PF00019; TGF_beta; 1.
 DR Pfam; PF00688; TGF_beta; 1.
 DR PRINTS; PR00438; GRCYSKNOT.
 DR PRODOM; PD000357; TGF_beta; 1.
 DR SMART; SM00204; TGF_beta; 1.
 DR PROSITE; PS00250; TGF_beta; 1.
 KW Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW Glycoprotein.
 FT SIGNAL 1 30
 FT PROPEP 31 322
 FT CHAIN 323 454
 FT DISULFID 353 419
 FT DISULFID 382 451
 FT DISULFID 386 453
 FT DISULFID 418 418
 FT CARBOHYD 211 211
 FT CARBOHYD 327 327
 FT CARBOHYD 345 345
 FT CARBOHYD 395 395
 SQ SEQUENCE 454 AA; 51736 MW; 63127413CC22EE CRC64;
 Query Match 78.4%; Score 87; DB 1; Length 454;
 Best Local Similarity 83.3%; Pred. No. 1,2e-05;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 PETVPRKPCCAPTQNLNALS 20
 DB 411 PDHVPKPCCAPTQNLNALS 428
 RESULT 9
 ID 60A_DROVI STANDARD; PRT; 436 AA.
 AC Q24735;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-OCT-2001 (Rel. 40, Last annotation update)
 DE 60A protein precursor (Glass bottom boat protein).
 GN GBS OR 60A OR TGF-beta-60A.
 OS Drosophila virilis (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96305349; PubMed=8688461;
 RA Du W., Doctor J.S.;
 RT "Isolation and sequence of the Drosophila virilis 60 A gene, a
 RT transforming growth factor-beta superfamily member related to
 RT vertebrate bone morphogenetic proteins.";
 RL Biochim. Biophys. Acta 1307:273-279(1996).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
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DR EMBL; U48595; AAC47262.1; -
 DR HSSP; P18075; 1BMP.
 DR Flybase; FBgn0015681; Dv1rYgbb.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein; Signal.
 KW SIGNAL
 FT PROPEP 1
 FT CHAIN 28
 FT DISULFID 318 436
 FT DISULFID 335 401
 FT DISULFID 364 433
 FT DISULFID 368 435
 FT DISULFID 400 400
 FT CARBOHYD 102 102
 FT CARBOHYD 114 114
 FT CARBOHYD 217 217
 FT CARBOHYD 229 229
 FT CARBOHYD 377 377
 SQ SEQUENCE 436 AA; 49999 MW; C744BAE58796692 CRC64;

Query Match 69.4%; Score 77; DB 1; Length 436;
 Best Local Similarity 63.2%; Pred. No. 0.00035;
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

DY 1 INPETYPRKCCAPTDLNAI 19
 DB 391 LEPKRVKPCCAPTRIGAL 409

RESULT 10
 60A_DROME STANDARD; PRT; 455 AA.

AC P27091; Q9W114;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 10-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 60A protein precursor (Glass bottom boat protein).
 GN GBB OR 60A OR TGFb-60A OR CG5562.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
 OC Ephydrozoa; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RX MEDLINE; 92201021; PubMed; 1924384;
 RA Wharton K.A., Thomson G.H., Gelbart W.M.,
 RT "Drosophila 60A gene, another transforming growth factor beta family
 RT member, is closely related to human bone morphogenetic proteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9214-9218(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 92290120; PubMed; 1601181;
 RA Doctor U.S., Jackson P.D., Rasnka K.E., Visalli M., Hoffmann F.M.,
 RT "Sequence, biochemical characterization, and developmental expression
 RT of a new member of the TGF-beta superfamily in Drosophila
 RT melanogaster";
 RL Dev. Biol. 151:491-505(1992).
 RN [3]
 RP SEQUENCE FROM N.A.

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DR EMBL; M77012; AAA28306.1; -
 DR EMBL; M84795; AAA28307.1; -
 DR EMBL; AE003462; AAF47075.1; -
 DR PIR; A43918; A43918.
 DR HSSP; P18075; 1BMP.
 DR Flybase; FBgn0024234; gbb.
 DR GO; GO:0008586; P:wing vein morphogenesis; IMP.
 DR GO; GO:0007474; P:wing vein specification; IMP.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGFb-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1
 36
 FT SIGNAL

STRAIN=Berkley;
 MEDLINE=20196007; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaralides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Chao M., Peiffer B.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolintsov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brooks-Pollock P., Brotler P.,
 RA Burdits K.C., Busam D.A., Butler H., Cadieu E., Canter A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davidson L.B., Davies P.,
 RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.V., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jalali M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- DEVELOPMENTAL STAGE: Expressed throughout development with peaks
 CC of transcription during early embryogenesis, in pupae, and in
 CC adult males.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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FT PROPEP 37 335 POTENTIAL.
 FT CHAIN 336 455 60A PROTEIN.
 FT DISULFID 354 420 BY SIMILARITY.
 FT DISULFID 383 452 BY SIMILARITY.
 FT DISULFID 387 454 BY SIMILARITY.
 FT DISULFID 419 419 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 455 AA; 51687 MW; C8FA79556341F94 CRC64;

Query Match 69.4%; Score 77; DB 1; Length 455;
 Best Local Similarity 63.2%; Pred. No. 0.0036;
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPETYKPCCAPTQJNAL 19
 Db 410 LEKRVKPCCAPTRLGAL 428

RESULT 11
 BMA_MOUSE
 ID BMA_MOUSE STANDARD; PRT; 399 AA.

AC P3481; 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-FEB-1994 (Rel. 28, Last annotation update)
 DE Bone morphogenetic protein 8A precursor (BMP-8A) (Osteogenic protein 2) (OP-2).
 GN BMP8A OR BMP8 OR BMP-8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=93094231; PubMed=1460021;
 RA Oezkaynak E., Schlegelsberg P.N.U., Jin D.F., Clifford G.M., Warren F.D., Diller E.A., Oppermann H.;
 RT "Osteogenic protein-2. A new member of the transforming growth factor-beta superfamily expressed early in embryogenesis.";
 RT J. Biol. Chem. 267:25220-25227(1992).
 CC -1- FUNCTION: Induces cartilage and bone formation. May be the osteoinductive factor responsible for the phenomenon of epithelial osteogenesis. Plays a role in calcium regulation and bone homeostasis (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- DEVELOPMENTAL STAGE: EXTENSIVE EXPRESSION FOUND IN 8-DAY EMBRYOS, PRL DRASTICALLY IN 10-DAY EMBRYOS AND VIRTUALLY ABSENT IN 17-DAY EMBRYOS.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
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 CC EMBL; M97017; AAB01365.1; -
 DR HSSP; P18075; IBMF.
 DR MGD; MGT104515; Bmp8a.
 DR GO; GO:0007283; P_spermatogenesis; IMP.
 DR InterPro; IPR002400; GF_CysKnot.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PRO0438; TGFbSKNOT.
 DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_beta_1; 1.
 KW Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis; Glycoprotein.

FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 260 POTENTIAL.
 FT CHAIN 261 399 BONE MORPHOGENETIC PROTEIN 8A.
 FT DISULFID 298 364 BY SIMILARITY.
 FT DISULFID 327 396 BY SIMILARITY.
 FT DISULFID 331 396 BY SIMILARITY.
 FT DISULFID 363 363 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 399 AA; 44764 MW; B7SFE32D5125E40C CRC64;

Query Match 64.9%; Score 72; DB 1; Length 399;
 Best Local Similarity 60.0%; Pred. No. 0.0018;
 Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 INPETYKPCCAPTQJNALIS 20
 Db 354 MKPDVVPKACAPTKLSTATS 373

RESULT 12
 DECA_DROPS
 ID DECA_DROPS STANDARD; PRT; 621 AA.

AC P91699; 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Decapentaplegic protein precursor (DPP-C protein).
 GN DPP.
 OS Drosophila pseudoobscura (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97225212; PubMed=9071585;
 RX Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M., de Cuevas M., Gelbart W.M.;
 RA "Molecular evolution at the decapentaplegic locus in Drosophila."; Genetics 145:297-309(1997).
 CC -1- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS TOGETHER WITH SCW (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP ARE INTERPRETIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: Expressed in the imaginal discs associated with establishment of the proximal-distal axis of the appendages, and midgut mesoderm (By similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
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 CC EMBL; U63856; AAC47553.1; -
 DR HSSP; P12643; BMP.
 DR FlyBase; FBgn0018547; Dpse\dp.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.

DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00668; TGFb propeptide; 1.
 DR PRINTS; PRO0668; INHIBINA.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
 KM Signal.
 FT SIGNAL. 1 15
 FT PROPEP 16 479
 FT CHAIN 480 621
 FT DISULFID 520 586
 FT DISULFID 549 618
 FT DISULFID 553 620
 FT DISULFID 585 585
 FT DOMAIN 45 57
 FT DOMAIN 88 92
 FT DOMAIN 95 104
 FT DOMAIN 163 173
 FT DOMAIN 483 495
 FT CARBOHYD 149 149
 FT CARBOHYD 365 365
 FT CARBOHYD 400 400
 FT CARBOHYD 562 562
 SQ SEQUENCE 621 AA; 69038 MW; 3FD714FB5509651 CRC64;
 Query Match 64.9%; Score 72; DB 1; Length 621;
 Best Local Similarity 55.0%; Pred. No. 0.0028; 4; Indels 0; Gaps 0;
 Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 INPETYKPCCAPTQLNIAIS 20
 DB 576 INPGKVPKACVPTQDSVA 595
 RESULT 13
 DVRT1_XENLA STANDARD; PRT; 360 AA.
 AC P09534;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE DVRT-1 protein precursor (Vegetal hemisphere Vg1 protein) (VG-1).
 GN DVRT-1 OR Vg1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8052889; PubMed=3479264;
 RA Weeks D.L., Melton D.A.;
 RT "A maternal mRNA localized to the vegetal hemisphere in Xenopus eggs
 codes for a growth factor related to TGF-beta.";
 RL Cell 51:861-867(1987).
 RN [2]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=89305504; PubMed=2519512;
 RA Dale L., Matthews G., Tabe L., Colman A.;
 RT "Developmental expression of the protein product of Vg1, a localized
 maternal mRNA in the frog Xenopus laevis.";
 RL EMBO J. 8:1057-1065(1989).
 CC -1- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER
 MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE
 SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
 CC -1- SUBUNIT: Homodimer (probable).
 CC -1- TISSUE SPECIFICITY: VEGETAL REGION OF THE EGG.
 CC -1- DEVELOPMENTAL STAGE: ABUNDANT IN OOCYTES AND PRESENT THROUGHOUT
 CLEAVAGE AND GASTRULA STAGE. NOT READILY DETECTED AT A STAGE WHEN
 SOMITOGENESIS IS NEARLY COMPLETE. IN 24 HR EMBRYOS, STEADY STATE
 LEVEL DECREASES IN A CONTINUOUS PASHION WITH DEVELOPMENTAL AGE.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.

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 CC -----
 DR EMBL; M18055; AA49727.1; -
 DR PIR; A29619; A29619.
 DR HSSP; P12643; 3BMP.
 DR InterPro; IPR002400; GF_cysknoc.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00668; TGFb_propeptide; 1.
 DR PRINTS; PRO0438; GF_CYSKNOC.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 KM Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 246
 FT CHAIN 247 360
 FT DISULFID 259 325
 FT DISULFID 288 357
 FT DISULFID 292 359
 FT DISULFID 324 324
 FT CARBOHYD 113 113
 FT CARBOHYD 181 181
 FT CARBOHYD 301 301
 SQ SEQUENCE 360 AA; 41772 MW; B44A18AA2750984 CRC64;
 Query Match 64.0%; Score 71; DB 1; Length 360;
 Best Local Similarity 55.0%; Pred. No. 0.0022; 5; Indels 0; Gaps 0;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 INPETYKPCCAPTQLNIAIS 20
 DB 315 IEPDIPPCVPTQMSPIIS 334
 RESULT 14
 BMB8_MOUSE STANDARD; PRT; 399 AA.
 AC P55105;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 8B precursor (BMP-8B).
 GN BMB8B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ICR; TISSUE=Placenta;
 RX MEDLINE=97000308; PubMed=8643393;
 RA Zhao G.Q., Hogan B.L.;
 RT "Evidence that mouse Bmp8a (Op2) and Bmp8b are duplicated genes that
 play a role in spermatogenesis and placental development.";
 RL Mech. Dev. 57:159-168(1996).
 CC -1- FUNCTION: Induces cartilage and bone formation. May be the
 CC osteoinductive factor responsible for the phenomenon of epithelial
 CC homeostasis (by similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
 CC -1- SIMILARITY: Belongs to the TGF-beta family.

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DR EMBL; U39545; AAB17573.1; -
 DR HSSP; P18075; BMP.
 DR MGD; MGI:107335; Bmpb.
 DR GO; GO:0007283; P:spermatogenesis; IMP.
 DR InterPro; IPR001839; TGFb N.
 DR InterPro; IPR001111; TGFb N.
 DR Pfam; PF000019; TGF-beta; I.
 DR Pfam; PF00688; TGF-beta; I.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF-beta; 1.
 KW Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW Glycoprotein.
 FT SIGNAL 1 19
 FT PROPEP 20 260
 FT CHAIN 261 399
 FT DISULFID 298 364
 FT DISULFID 327 396
 FT DISULFID 331 398
 FT DISULFID 363 363
 FT CARBOHYD 155 155
 FT CARBOHYD 340 340
 SQ SEQUENCE 399 AA; 44752 MW; EFAOBV88C7EC4839 CR664;

Query Match 64.0%; Score 71; DB 1; Length 399;
 Best Local Similarity 55.0%; Pred. No. 0.0025;
 Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 INPETYKPCAPQTQINAI 20
 DB 354 MKPDIIPKVCVPELISAIS 373

DECA_DROME STANDARD; PRT; 588 AA.
 ID DECA_DROME P07713; P91651;
 AC P07713; P91651;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Decapentaplegic protein precursor (Dpp-C protein).
 GN DPP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87090408; PubMed=3467201;
 RA Padgett R.W., St Johnston R.D., Gelbart W.M.;
 RT "A transcript from a Drosophila pattern gene predicts a protein
 RT homologous to the transforming growth factor-beta family";
 RL Nature 325:81-84(1987).
 RP [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=DF CN BM;
 RX MEDLINE=97225213; PubMed=9071586;
 RA Richter B., Long M., Lewontin R.C., Nitasaka E.;
 RT "Nucleotide variation and conservation at the dpp locus, a gene
 RT controlling early development in Drosophila";
 RL Genetics 145:311-323(1997).
 RP [3]
 RP CHARACTERIZATION, AND SEQUENCE OF 457-476.

FX MEDLINE=90258853; PubMed=1692958;
 RA Panganiban G.E.F., Rashka K.E., Netzel M.D., Hoffmann F.M.;
 RT "Biochemical characterization of the Drosophila dpp protein, a member
 RT of the transforming growth factor beta family of growth factors";
 RL Mol. Cell. Biol. 10:2669-2677(1990).
 CC -1- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
 CC TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
 CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
 CC EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
 CC VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
 CC TOGETHER WITH SCW.
 CC -1- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT. DPP/DPP
 CC HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
 CC ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN.
 CC -1- TISSUE SPECIFICITY: Expressed in the imaginal discs associated
 CC with establishment of the proximal-distal axis of the appendages,
 CC and midgut mesoderm.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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DR EMBL; M30116; AAA28482.1; -
 DR PIR; A26158; A26158.
 DR HSSP; P12643; 3BMP.
 DR FlyBase; FBgn0000490; dpp.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR GO; GO:0005622; C:intracellular; IDA.
 DR GO; GO:0016015; F:morphogen activity; NAS.
 DR GO; GO:0005160; F:transforming growth factor-beta receptor bi.; NAS.
 DR GO; GO:0007378; P:amniogenesis formation; NAS.
 DR GO; GO:0007448; P:anterior/posterior pattern formation; NAS.
 DR GO; GO:0007391; P:dorsal closure; NAS.
 DR GO; GO:0001715; P:ectoderm cell fate specification; NAS.
 DR GO; GO:0007483; P:genital disc metamorphosis; NAS.
 DR GO; GO:0007442; P:hindgut morphogenesis; NAS.
 DR GO; GO:0007560; P:imaginal disc morphogenesis; NAS.
 DR GO; GO:0007479; P:leg disc proximal/distal pattern formation; NAS.
 DR GO; GO:0042127; P:regulation of cell proliferation; NAS.
 DR GO; GO:0019827; P:stem cell maintenance; NAS.
 DR GO; GO:0007179; P:TGF-beta receptor signaling pathway; NAS.
 DR GO; GO:0007425; P:tracheal cell fate determination (sensu ins. .); NAS.
 DR GO; GO:0008586; P:wing vein morphogenesis; IMP.
 DR GO; GO:0007474; P:wing vein specification; IMP.
 DR GO; GO:0007352; P:zygotic determination of dorsal/ventral axis; NAS.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb N.
 DR InterPro; IPR001111; TGFb N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb-propeptide; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF-beta; 1.
 KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
 KW Signal.
 FT SIGNAL 1 15
 FT PROPEP 16 456
 FT CHAIN 457 588
 FT DISULFID 487 553
 FT DISULFID 516 585
 FT DISULFID 520 587
 FT DISULFID 552 552
 FT CARBOHYD 120 120
 FT CARBOHYD 342 342
 FT CARBOHYD 377 377
 FT CARBOHYD 529 529

DECAPENTAPLEGIC PROTEIN.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 INTERCHAIN (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 59 59 V -> G (IN STRAIN DP CN BW).
 FT VARIANT 121 121 K -> M (IN STRAIN DP CN BW).
 FT VARIANT 473 474 HA -> QP (IN STRAIN DP CN BW).
 SQ SEQUENCE 588 AA; 65850 MW; 3D986A7DF5DF666B CRC64;

Query Match 64.0%; Score 71; DB 1; Length 588;
 Best Local Similarity 55.0%; Pred. No. 0.0037;
 Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 INPETYKPCCAPTOLNALS 20
 Db 543 MNPCKVFKACVPTQLDSVA 562

Search completed: October 12, 2004, 09:34:23
 Job time : 20 secs

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